

## SEQUENCE LISTING

<110> Lee, Bruce Andrew Flores, Becky Mar Valkirs, Gunars Edwin Biosite Diagnostics, Inc.

<120> Assays for Detection of Bacillus Anthracis

<130> 014907-003310US

<140> US 09/754,947

<141> 2001-01-04

<150> US 60/174,901

<151> 2000-01-06

<160> 5

<170> PatentIn Ver. 2.1

<210> 1

<211> 785

<212> PRT

<213> Bacillus anthracis

<220>

<223> surface array protein (SAP)

<400> 1

Ala Gly Lys Thr Phe Pro Asp Val Pro Ala Asp His Trp Gly Ile Asp 1 5 10 15

Ser Ile Asn Tyr Leu Val Glu Lys Gly Ala Val Lys Gly Asn Asp Lys 20 25 30

Gly Met Phe Glu Pro Gly Lys Glu Leu Thr Arg Ala Glu Ala Ala Thr 35 40 45

Met Met Ala Gln Ile Leu Asn Leu Pro Ile Asp Lys Asp Ala Lys Pro 50 55 60

Ser Phe Ala Asp Ser Gln Gly Gln Trp Tyr Thr Pro Phe Ile Ala Ala 65 70 75 80

Val Glu Lys Ala Gly Val Ile Lys Gly Thr Gly Asn Gly Phe Glu Pro 85 90 95

Asn Gly Lys Ile Asp Arg Val Ser Met Ala Ser Leu Leu Val Glu Ala 100 105 110

Tyr Lys Leu Asp Thr Lys Val Asn Gly Thr Pro Ala Thr Lys Phe Lys 115 120 125

Asp Leu Glu Thr Leu Asn Trp Gly Lys Glu Lys Ala Asn Ile Leu Val

Glu Leu Gly Ile Ser Val Gly Thr Gly Asp Gln Trp Glu Pro Lys Lys 145 150 155 160

 $00^{3}$ 

Thr Val Thr Lys Ala Glu Ala Ala Gln Phe Ile Ala Lys Thr Asp Lys 165 170 175

Gln Phe Gly Thr Glu Ala Ala Lys Val Glu Ser Ala Lys Ala Val Thr 180 185 190

Thr Gln Lys Val Glu Val Lys Phe Ser Lys Ala Val Glu Lys Leu Thr

Lys Glu Asp Ile Lys Val Thr Asn Lys Ala Asn Asn Asp Lys Val Leu 210 215 220

Val Lys Glu Val Thr Leu Ser Glu Asp Lys Arg Ser Ala Thr Val Glu 225 230 235 240

Leu Tyr Ser Asn Leu Ala Ala Lys Gln Thr Tyr Thr Val Asp Val Asn 245 250 255

Lys Val Gly Lys Thr Glu Val Ala Val Gly Ser Leu Glu Ala Lys Thr 260 265 270

Ile Glu Met Ala Asp Gln Thr Val Val Ala Asp Glu Pro Thr Ala Leu 275 280 285

Gln Phe Thr Val Lys Asp Glu Asn Gly Thr Glu Val Val Ser Pro Glu 290 295 300

Gly Ile Glu Phe Val Thr Pro Ala Ala Glu Lys Ile Asn Ala Lys Gly 305 310 315 320

Glu Ile Thr Leu Ala Lys Gly Thr Ser Thr Thr Val Lys Ala Val Tyr 325 330 335

Lys Lys Asp Gly Lys Val Val Ala Glu Ser Lys Glu Val Lys Val Ser 340 345 350

Ala Glu Gly Ala Ala Val Ala Ser Ile Ser Asn Trp Thr Val Ala Glu 355 360 365

Gln Asn Lys Ala Asp Phe Thr Ser Lys Asp Phe Lys Gln Asn Asn Lys 370 375 380

Val Tyr Glu Gly Asp Asn Ala Tyr Val Gln Val Glu Leu Lys Asp Gln 385 390 395 400

Phe Asn Ala Val Thr Thr Gly Lys Val Glu Tyr Glu Ser Leu Asn Thr 405 410 415

Glu Val Ala Val Asp Lys Ala Thr Gly Lys Val Thr Val Leu Ser
420 425 430

Ala Gly Lys Ala Pro Val Lys Val Thr Val Lys Asp Ser Lys Gly Lys 435 440 445

Ala Leu Val Ser His Thr Val Glu Ile Glu Ala Phe Ala Gln Lys Ala 450 455 460

Met Lys Asp Ile Lys Leu Glu Lys Thr Asn Val Ala Leu Ser Thr Lys 465 470 475 480

Asp Val Thr Asp Leu Lys Val Lys Ala Pro Val Leu Asp Gln Tyr Gly
485 490 495

Lys Glu Phe Thr Ala Pro Val Thr Val Lys Val Leu Asp Lys Asp Gly 500 505 510

Lys Glu Leu Lys Glu Gln Lys Leu Glu Ala Lys Tyr Val Asn Arg Glu 515 520 525

Leu Val Leu Asn Ala Ala Gly Gln Glu Ala Gly Asn Tyr Thr Val Val 530 535 540

Leu Thr Ala Lys Ser Gly Glu Lys Glu Ala Lys Ala Thr Leu Ala Leu 545 550 555 560

Glu Leu Lys Ala Pro Gly Ala Phe Ser Lys Phe Glu Val Arg Gly Leu 565 570 575

Asp Thr Glu Leu Asp Lys Tyr Val Thr Glu Glu Asn Gln Lys Asn Ala 580 585 590

Met Thr Val Ser Val Leu Pro Val Asp Ala Asn Gly Leu Val Leu Lys 595 600 605

Gly Ala Glu Ala Ala Glu Leu Lys Val Thr Thr Thr Asn Lys Glu Gly 610 615 620

Lys Glu Val Asp Ala Thr Asp Ala Gln Val Thr Val Gln Asn Asn Ser 625 630 635 640

Val Ile Thr Val Gly Gln Gly Ala Lys Ala Gly Glu Thr Tyr Lys Val 645 650 655

Thr Val Val Leu Asp Gly Lys Leu Ile Thr Thr His Ser Phe Lys Val 660 665 670

Val Asp Thr Ala Pro Thr Ala Lys Gly Leu Ala Val Glu Phe Thr Ser 675 680 685

Thr Ser Leu Lys Glu Val Ala Pro Asn Ala Asp Leu Lys Ala Ala Leu 690 700

Leu Asn Ile Leu Ser Val Asp Gly Val Pro Ala Thr Thr Ala Lys Ala 705 710 715 720

Thr Ala Ser Asn Val Glu Phe Val Ser Ala Asp Thr Asn Val Val Ala
725 730 735

Glu Asn Gly Thr Val Gly Ala Lys Gly Ala Thr Ser Ile Tyr Val Lys 740 745 750

Asn Leu Thr Val Val Lys Asp Gly Lys Glu Gln Lys Val Glu Phe Asp 755 760 765

Lys Ala Val Gln Val Ala Val Ser Ile Lys Glu Ala Lys Pro Ala Thr 770 775 780

Lys 785

(N)3

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<212> DNA
<213> Bacillus anthracis
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<223> surface array protein (SAP)
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gaaaaggcg cagttaaagg taacgacaaa
cgtgcagaag cagctacaat gatggctcaa

aaaacattcc cagacgttcc tgctgatcac tggggaattg attccattaa ctacttagta 60 gaaaaaggcg cagttaaagg taacgacaaa ggaatgttcg agcctggaaa agaattaact 120 cgtgcagaag cagctacaat gatggctcaa atcttaaact taccaatcga taaagatgct 180 aaaccatctt tcgctgactc tcaaggccaa tggtacactc cattcatcgc agctgtagaa 240 aaagctggcg ttattaaagg tacaggaaac ggctttgagc caaacggaaa aatcgaccgc 300 gtttctatgg catctcttct tgtagaagct tacaaattag atactaaagt aaacggtact 360 ccagcaacta aattcaaaga tttagaaaca ttaaactggg gtaaagaaaa agctaacatc 420 ttagttgaat taggaatete tgttggtaet ggtgateaat gggageetaa gaaaaetgta 480 actaaagcag aagctgctca attcattgct aagactgaca agcagttcgg tacagaagca 540 qcaaaaqttq aatctqcaaa agctgttaca actcaaaaag tagaagttaa attcagcaaa 600 qctqttqaaa aattaactaa aqaaqatatc aaagtaacta acaaagctaa caacgataaa 660 gtactagtta aagaggtaac tttatcagaa gataaaagat ctgctacagt tgaattatat 720 aqtaacttaq cagctaaaca aacttacact gtagatgtaa acaaagttgg taaaacagaa 780 gtagctgtag gttctttaga agcaaaaaca atcgaaatgg ctgaccaaac agttgtagct 840 gatgagccaa cagcattaca attcacagtt aaagatgaaa acggtactga agttgtttca 900 ccagagggta ttgaatttgt aacgccagct gcagaaaaaa ttaatgcaaa aggtgaaatc 960 actttagcaa aaggtacttc aactactgta aaagctgttt ataaaaaaaga cggtaaagta 1020 gtagctgaaa gtaaagaagt aaaagtttct gctgaaggtg ctgcagtagc ttcaatctct 1080 aactggacag ttgcagaaca aaataaagct gactttactt ctaaagattt caaacaaaac 1140 aataaagttt acgaaggcga caacgcttac gttcaagtag aattgaaaga tcaatttaac 1200 gcagtaacaa ctggaaaagt tgaatatgag tcgttaaaca cagaagttgc tgtagtagat 1260 aaagctactg gtaaagtaac tgtattatct gcaggaaaag caccagtaaa agtaactgta 1320 aaagattcaa aaggtaaagc acttgtttca cacacagttg aaattgaagc tttcgctcaa 1380 aaagcaatga aagacattaa attagaaaaa actaacgtag cgctttctac aaaagatgta 1440 acagatttaa aagtaaaagc tccagtacta gatcaatacg gtaaagagtt tacagctcct 1500 gtaacagtga aagtacttga taaagatggt aaagaattaa aagaacaaaa attagaagct 1560 aaatatgtga acagagaatt agttctgaat gcagcaggtc aagaagctgg taattataca 1620 gttgtattaa ctgcaaaatc tggtgaaaaa gaagcaaaag ctacattagc tctagaatta 1680 aaagctccag gtgcattctc taaatttgaa gttcgtggtt tagacacaga attagataaa 1740 tatgttactg aggaaaacca aaagaatgca atgactgttt cagttcttcc tgtagatgca 1800 aatggattag tattaaaagg tgcagaagca gctgaactaa aagtaacaac aacaaacaaa 1860 gaaggtaaag aagtagacgc aactgatgca caagttactg tacaaaataa cagtgtaatt 1920 actgttggtc aaggtgcaaa agctggtgag acttataaag taacagttgt actagatggt 1980 aaattaatca caactcattc attcaaagtt gttgatacag caccaactgc taaaggatta 2040 gcagtagaat ttacaagcac atctcttaaa gaagtagctc caaatgctga tttaaaagct 2100 gcacttttaa atatettate tgttgatggt gtacetgega etacageaaa ageaacaget 2160 tctaatgtag aatttgtttc tgctgacaca aatgttgtag ctgaaaatgg tacagttggt 2220 gcaaaaggtg caacatctat ctatgtgaaa aacctgacag ttgtaaaaga tggaaaagag 2280 caaaaagtag aatttgataa agctgtacaa gttgcagttt ctattaaaga agcaaaacct 2340 gcaacaaaac atcaccatca ccatcactaa 2370

0

<210> 3

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:5' PCR primer

<400> 3

tcgctgccca accagccatg gccgcaggta aaacattccc agac

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<210> 4
<211> 89
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<213> Artificial Sequence
<223> Description of Artificial Sequence:3' PCR primer
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gtgataaact accgcattaa agcttatcga tgataagctg tcaattagtg atggtgatgg 60
tgatgttttg ttgcaggttt tgcttcttt
<210> 5
<211> 201
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: flexible linker
<220>
<221> MOD_RES
<222> (1)..(97)
<223> Gly at positions 1-97 may be present or absent
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<221> MOD RES
<222> (105)..(201)
<223> Gly at positions 105-201 may be present or absent
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75
          70
65
110
      100
               105
120
130
            135
                     140
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155

160

145

150

